Inferring the clinical severity of COVID-19 during Australia's Delta wave

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Introduction

Since early 2020, all of our lives have been impacted by COVID-19. This novel infectious disease has overwhelmed health care system around the world. In this project, we aim to fit a hospital progression model with time-series data of the Delta wave (from 1/6/2021 to 15/11/2021) in Australia via Approximate Bayesian Computation (ABC).

Model Description

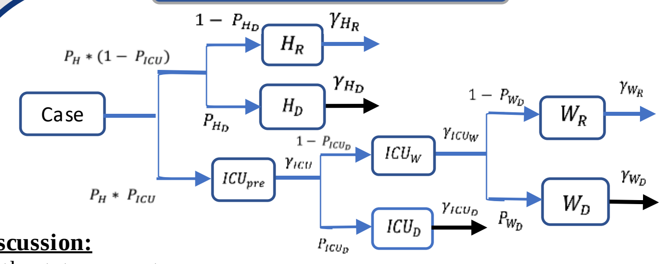


Figure 1. Hospital progression model

Table 1. Descriptions of all states and transitions in the model

State(X)	Description
pre	General admission before step-up to ICU
H_D	General ward before death in general ward
H_R	General ward before discharge from general ward
ICU_D	ICU before death in ICU
ICU_W	ICU before step-down care
W_D	Step-down (general ward) before death
W_R	Step-down (general ward) before discharge
Transition(Z)	**Description**
H	Get into hospital from general cases
ICU	Admission to ICU from general ward
H_D	Death in general ward
ICU_D	Death in ICU
W_D	Death in step-down care

Discussion:

All the state parameters were assumed to be fixed with the values that were referenced from [1] during the simulation. It is worth mentioning that all the transition parameters that fitted to the England SARS-CoV-2 epidemic model [1] will not fit the Australian data. This is because England has a different number of immunities, different stages of vaccination, and a different system of hospitalization compared to Australia, which indicates that the susceptibility to severe COVID-19 may look very different between these two countries. As a result, **we wish to infer the transition parameters** using Approximate Bayesian Computation Markov Chain Monte Carlo (ABC-MCMC) to fit the local data.

Reference

1. Edward, K, Lilith, W & John, A 2021, 'Key epidemiological drivers and impact of interventions in the 2020 SARS-CoV-2 epidemic in England', *Science Translational Medicine*, vol. 13, no. 602, Doi: 10.1126/scitranslmed.abg4262.

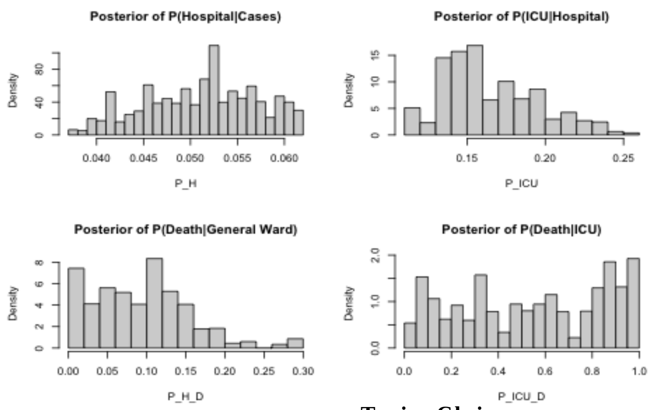
ABC-MCMC

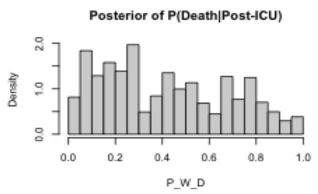
Consider Bayesian inference for parameter vector θ under a model with density $\pi(\boldsymbol{y}|\theta)$. Let $\pi(\theta)$ be the prior density and $\boldsymbol{y}_{\text{obs}}$ represent the observed data. It is assumed that $\pi(\boldsymbol{y}|\theta)$ cannot easily be evaluated but that it is straightforward to sample from the model. ABC-MCMC (Algorithm 1) exploits this to sample from an approximation to the posterior density $\pi(\theta|\boldsymbol{y})$. It requires several tuning choices: number of simulations N, a threshold $h \geq 0$, a function $S(\boldsymbol{y})$ mapping data to a vector of summary statistics, and a distance function $d(\cdot,\cdot)$. We consider a simplified version of the ABC-MCMC algorithm for Uniform priors and a symmetric proposal density.

Algorithm 1 Simplified ABC-MCMC

```
Sample θ⁰ ~ Unif(0,1), x⁰ ~ π(y|θ⁰) until φ⁰ = 𝕀{d(y,x⁰)≤h} = 1
for i = 1 to N do
    Draw θ*~q(·|θ^{i−1}), simulate x* ~ f(·|θ*), and compute φ* = 𝕀{d(y,x*)≤h}
    if φ* = 1 then θ^i = θ*
    else θ^i = θ^{i−1}
    end if
end for
```

Posterior Distributions





Tuning Choices:

Number of Simulations: 100,000
Distance Function: Residual Sum of Squares
Threshold for Ward Occupancy: 100
Threshold for ICU Occupancy: 30
Threshold for Daily Deaths: 10
Prior Distribution: Uniform(0, 1)
Proposal Distribution: Normal($\boldsymbol{\theta}^{i-1}$, 0.1)

Figure 2. Posterior distributions of the transition parameters

Simulation Results

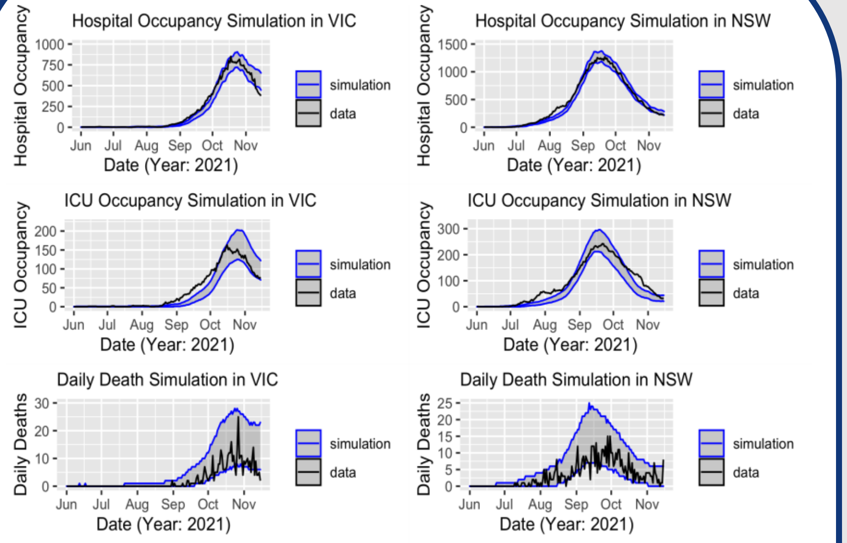


Figure 3. Simulation results of VIC & NSW

Methodology & Conclusion:

Figure 3 illustrates the simulation results of VIC & NSW by randomly sampling 1000 sets of parameters from the posterior distributions (Figure 2), and then simulating the result using these parameter sets. After that, choose 5% quantile as the lower bound, and 95% quantile as the upper bound. These simulations were used to form a 90% confidence region. It can be seen that these regions can cover most of the data which indicates that the hospital progression model is fitted well with the local data after ABC-MCMC. This model can be further used for predicting the clinical outcomes of Delta infection down the line and making comparisons to the Omicron for the purpose of obtaining valuable information for society.

Acknowledgements

I would like to say a special thank you to my supervisor Dr. James Walker for their patient guidance, expert advice, and inspiring encouragement throughout this project. I would also like to thank the Vacation Scholarship Program for offering me such an invaluable opportunity to help me getting start on my research journey.

Further Information

GitHub: https://github.com/JamesZhang0202/2022VocationScholarship